**DOCKET NO.:** HENK-0060 / H4714

**Application No.: 10/774,018** 

Preliminary Amendment - First Action Not Yet Received

Amendments to the Specification:

Please amend the first paragraph following title as follows:

-- CROSS-REFERENCE TO RELATED APPLICATIONS

This is application is a continuation of International Application No. PCT/EP02/08391, filed July 27, 2002, which claims priority to German Application No. DE 101 38 753.9, filed August 7, 2001, all of which are incorporated herein by reference in their entireties.--

**PATENT** 

Please insert the Sequence Listing being filed concurrently herewith into the specification.

Please amend the paragraph spanning page 20, line 30 to page 21, line 2 as follows:

-- If any uncertainties with respect to the numbering should arise from contemplating the amino acid sequences, then the corresponding nucleotide sequence (e.g., one of SEQ ID NOs:5, 7, 9, 11, 13, 15 and 17) as disclosed in the sequence listing is decisive, since the formation of hybrid proteins advantageously takes place at the level of the corresponding DNA. The number of the point of fusion thus results from the number of the codon downstream of whose first, second or third nucleobase the switch to the other DNA has occurred, again in each case with respect to the codon numbering of *B. amyloliquefaciens* (SEQ ID No 3).--

## Please amend the last full paragraph on page 94 at lines 18-34 as follows:

--Figure 2: Alignment of the amino acid sequences of the preproteins (precursors) of the α-amylases of *B. licheniformis* (B.L) (SEQ ID NO:19) and *B. amyloliquefaciens* (B.A.) (SEQ ID NO: 20).

The leader peptide of *B. licheniformis*  $\alpha$ -amylase comprises 29 amino acids and that of *B. amyloliquefaciens*  $\alpha$ -amylase 31. The mature proteins are in each case 483 amino acids in length.

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Highlighted in bold type are in each case the first amino acid of the mature protein and the amino acids corresponding to positions 19, 34, 76, 84, 112, 153, 256 and 433 in the counting of the mature *B. amyloliquefaciens* protein. The switches from the one to the other sequence downstream of one and, respectively, two of these positions characterize the in each case particularly preferred embodiments of the present invention.—